Genome-wide association mapping and comparative genomics identifies genomic regions governing grain nutritional traits in finger millet (Eleusine coracana L. Gaertn)

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Plants, People, Planet **Supporting Information**

Article title: **Genome-wide association mapping and comparative genomics identifies genomic regions governing grain nutritional traits in finger millet (*Eleusine coracana* L. Gaertn.)**

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The following Supporting Information is available for this article:

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Dataset S1 SNPs associated with grain micronutrients.

Table S1 The origin of 190 finger millet accessions used in this study.

Inventory	Acc name/number (IE)	Collection	Origin	Geographic Region
1	501	Minicore	India	Asia
2	518	Minicore	India	Asia
3	1055	Minicore	Unknown	Unknown
4	2034	Minicore	India	Asia
5	2042	Minicore	India	Asia
6	2217	Minicore	India	Asia
7	2296	Minicore	India	Asia
8	2312	Minicore	India	Asia
9	2430	Minicore	Kenya	East Africa
10	2437	Minicore	Kenya	East Africa
11	2457	Minicore	Kenya	East Africa
12	2589	Minicore	USA	America
13	2606	Minicore	Malawi	South Africa
14	2619	Minicore	Malawi	South Africa
15	2821	Minicore	Nepal	Asia
16	2871	Minicore	Zambia	South Africa
17	2872	Minicore	Zambia	South Africa
18	2911	Minicore	Zambia	South Africa
19	2957	Minicore	Germany	Europe
20	3045	Minicore	India	Asia
21	3077	Minicore	India	Asia
22	3104	Minicore	India	Asia
23	3317	Minicore	Zimbabwe	South Africa
24	3391	Minicore	Zimbabwe	South Africa
25	3392	Minicore	Zimbabwe	South Africa
26	3470	Minicore	India	Asia
27	3475	Minicore	India	Asia
28	3614	Minicore	Unknown	Unknown

29	3721	Minicore	Uganda	East Africa
30	3945	Minicore	Uganda	East Africa
31	3952	Minicore	Uganda	East Africa
32	3973	Minicore	Uganda	East Africa
33	4028	Minicore	Uganda	East Africa
34	4057	Minicore	Uganda	East Africa
35	4073	Minicore	Uganda	East Africa
36	4121	Minicore	Uganda	East Africa
37	4329	Minicore	Zimbabwe	South Africa
38	4491	Minicore	Zimbabwe	South Africa
39	4497	Minicore	Zimbabwe	South Africa
40	4545	Minicore	Zimbabwe	South Africa
41	4565	Minicore	Zimbabwe	South Africa
42	4570	Minicore	Zimbabwe	South Africa
43	4622	Minicore	Zimbabwe	South Africa
44	4646	Minicore	Zimbabwe	South Africa
45	4671	Minicore	India	Asia
46	4734	Minicore	India	Asia
47	4757	Minicore	India	Asia
48	4759	Minicore	India	Asia
49	4797	Minicore	Maldives	Asia
50	4816	Minicore	India	Asia
51	5066	Minicore	Senegal	West Africa
52	5091	Minicore	Zimbabwe	South Africa
53	5106	Minicore	Zimbabwe	South Africa
54	5201	Minicore	India	Asia
55	5306	Minicore	Zimbabwe	South Africa
56	5367	Minicore	Kenya	East Africa
57	5537	Minicore	Nepal	Asia
58	5870	Minicore	Nepal	Asia
59	6059	Minicore	Nepal	Asia

60	6154	Minicore	Nepal	Asia
61	6165	Minicore	Nepal	Asia
62	6221	Minicore	Nepal	Asia
63	6240	Minicore	Zimbabwe	South Africa
64	6294	Minicore	Zimbabwe	South Africa
65	6326	Minicore	Zimbabwe	South Africa
66	6337	Minicore	Zimbabwe	South Africa
67	6350	Minicore	Zimbabwe	South Africa
68	6421	Minicore	Uganda	East Africa
69	6473	Minicore	Uganda	East Africa
70	6514	Minicore	Zimbabwe	South Africa
71	6533	Minicore	Nigeria	West Africa
72	7018	Minicore	Kenya	East Africa
73	7081	Minicore	Kenya	East Africa
74	7320	Minicore	Kenya	East Africa
75	7508	Minicore	Ethiopia	East Africa
76	ACC#32	Elite local	Unknown	Unknown
77	Acc. # 29 FMB/01 WK	Elite local	Unknown	Unknown
78	Acc. # 32 FMB/01 WK	Elite local	Unknown	Unknown
79	Acc.# 25 FMB/01 WK	Elite local	Unknown	Unknown
80	AICSMIP # 3	Elite local	Unknown	Unknown
81	AICSMIP # 58	Elite local	Unknown	Unknown
82	AICSMIP # 9	Elite local	Unknown	Unknown
83	ENDING	Elite local	Uganda	East Africa
84	ENGENY	Elite local	Uganda	East Africa
85	Gulu E	Elite local	Uganda	East Africa
86	HR 374	Elite local	Unknown	Unknown
87	Ikhulule	Elite local	Kenya	East Africa
88	KNE # 1015	Elite local	Kenya	East Africa
89	KNE # 1034	Elite local	Kenya	East Africa
90	KNE # 1063	Elite local	Kenya	East Africa

91	KNE # 1124	Elite local	Kenya	East Africa
92	KNE # 1149	Elite local	Kenya	East Africa
93	KNE # 392	Elite local	Kenya	East Africa
94	KNE # 434	Elite local	Kenya	East Africa
95	KNE # 622	Elite local	Kenya	East Africa
96	KNE # 624	Elite local	Kenya	East Africa
97	KNE # 628	Elite local	Kenya	East Africa
98	KNE # 629	Elite local	Kenya	East Africa
99	KNE # 648	Elite local	Kenya	East Africa
100	KNE # 669	Elite local	Kenya	East Africa
101	KNE # 688	Elite local	Kenya	East Africa
102	KNE # 689	Elite local	Kenya	East Africa
103	KNE # 689	Elite local	Kenya	East Africa
104	KNE # 741	Elite local	Kenya	East Africa
105	KNE # 758	Elite local	Kenya	East Africa
106	KNE # 814	Elite local	Kenya	East Africa
107	KNE 1098	Elite local	Kenya	East Africa
108	KNE 409	Elite local	Kenya	East Africa
109	KNE 479	Elite local	Kenya	East Africa
110	KNE 796	Elite local	Kenya	East Africa
111	KNE 884	Elite local	Kenya	East Africa
112	Nakuru FM 1	Elite local	Kenya	East Africa
113	Okhale-1	Elite local	Nepal	Asia
114	P 224	Elite local	Uganda	East Africa
115	S # 414 GRU/ICRISAT	Elite local	Unknown	Unknown
116	S # 589 GRU/ICRISAT	Elite local	Unknown	Unknown
117	S # 70 SADC/ICRISAT	Elite local	Unknown	Unknown
118	S # 94 SDFM 1752	Elite local	Unknown	Unknown
119	SDFM 1702	Elite local	Unknown	Unknown
120	U 15	Elite local	Uganda	East Africa
121	Uganda Coll. # 3 Sel.10	Elite local	Uganda	East Africa

122	VL 137	Elite local	Unknown	Unknown
123	VL 224	Elite local	Unknown	Unknown
125	9	Core	India	Asia
126	61	Core	India	Asia
130	546	Core	India	Asia
134	595	Core	India	Asia
145	872	Core	Mexico	America
146	886	Core	Pakistan	Asia
152	1023	Core	Unknown	Unknown
155	2008	Core	India	Asia
166	2108	Core	India	Asia
182	2293	Core	India	Asia
185	2341	Core	Kenya	East Africa
187	2354	Core	Kenya	East Africa
203	2500	Core	Kenya	East Africa
209	2564	Core	Kenya	East Africa
214	2581	Core	Italy	Europe
215	2586	Core	Italy	Europe
216	2587	Core	Italy	Europe
219	2593	Core	USA	America
220	2608	Core	Malawi	South Africa
223	2644	Core	Malawi	South Africa
224	2645	Core	Malawi	South Africa
233	2760	Core	Malawi	South Africa
240	2825	Core	Tanzania	East Africa
241	2838	Core	India	Asia
246	2869	Core	Zambia	South Africa
249	2896	Core	Zambia	South Africa
253	2971	Core	Sri Lanka	Asia
254	2983	Core	Sri Lanka	Asia
259	3025	Core	Ethiopia	East Africa

260	3028	Core	India	Asia
261	3038	Core	India	Asia
262	3046	Core	India	Asia
263	3062	Core	India	Asia
264	3066	Core	India	Asia
265	3070	Core	India	Asia
266	3073	Core	India	Asia
275	3124	Core	India	Asia
283	3196	Core	Tanzania	East Africa
288	3257	Core	Zimbabwe	South Africa
302	3443	Core	Zimbabwe	South Africa
303	3449	Core	United Kingdom	Europe
304	3450	Core	United Kingdom	Europe
305	3455	Core	United Kingdom	Europe
306	3477	Core	Kenya	East Africa
308	3489	Core	Kenya	East Africa
309	3492	Core	Kenya	East Africa
331	3738	Core	Uganda	East Africa
362	4218	Core	Burundi	East Africa
363	4220	Core	Zimbabwe	South Africa
368	4287	Core	Zimbabwe	South Africa
394	4826	Core	India	Asia
401	4916	Core	Uganda	East Africa
415	5124	Core	India	Asia
440	5331	Core	India	Asia
455	5485	Core	India	Asia
459	5517	Core	Nepal	Asia
469	5672	Core	Nepal	Asia

491	5992	Core	Nepal	Asia
493	6013	Core	Nepal	Asia
496	6029	Core	Nepal	Asia
497	6033	Core	Nepal	Asia
502	6112	Core	Nepal	Asia
514	6300	Core	Zimbabwe	South Africa
515	6313	Core	Zimbabwe	South Africa
528	6528	Core	Zimbabwe	South Africa
529	6537	Core	Nigeria	West Africa
530	6541	Core	Nigeria	West Africa

Table S2 UNEAK/GBS TASSEL 3.0 Standalone pipeline arguments implemented in this study.

Pipeline	Plugin	Option	Value	Description	Purpose
UNEAK/GBS	FastqToTagCountPlugin	c	1	Minimum number of times a tag must be present in the raw sequence file to be output (Default: 1).	Converts raw sequences to tag counts
		s	300000000	Maximum good barcoded reads/ lane in a raw sequence file (Default: 300000000).	
UNEAK/GBS	MergeMultipleTagCountPlugin	c	3	Minimum number of times a tag must be present across the entire experiment to be output (Default: 1).	Merges tag counts and creates a master tag count file. Option removes rare or singleton tags that possibly result from sequencing errors
UNEAK/GBS	TagCountToFastqPlugin	c	3	Minimum count of reads across all samples for a tag to be output (Default: 1).	Creates a fastq file with unique 64 bp sequence tags for alignment to reference
UNEAK	UTagCountToTagPairPlugin	e	0.03	Error tolerance rate in the network filter (Default: 0.03).	Pairwise tag alignment to identify 'tag pairs' that differ by only 1 bp. Builds a homology network of tags to identify reciprocal tag pairs representing putative SNPs
UNEAK	UExportTagPairPlugin	d	100	(or --distance) distance to pad between each tag pairs by (Default: 1000).	Converts the 'tag pairs' file into a (fake) TOPM

					file for reintegration with GBS pipeline
External (UGENE)	When refence genome available	Indexed reference genome	N/A	Default	BWA alignment between tags and the refence genome
GBS	SAMConverterPlugin	N/A	N/A	Default	Converts the SAM file into a TOPM file for integration with GBS pipeline
UNEAK/GBS	FastqToTBTPlugin	y	N/A	output to tagsByTaxaByte (maximum 127 reads/tag/taxon) format instead of tagsByTaxaBit (0 or 1; tag absence or presence in a taxon) format.	Generates one TagsByTaxa (TBT) file per raw sequence file. Option stores the number of reads per tags per taxon to score heterozygotes & homozygotes quantitatively. Reduces false heterozygosity scoring due to sequencing errors
		e	ApeKI	Enzyme used to create the GBS library	
		c	1	Minimum taxa count within a raw sequencing file for a tag to be output. Default: 1.	Option removes tags that are present in the master tag count file but absent from the raw sequencing file
UNEAK/GBS	MergeTagsByTaxaFilesPlugin	s	300000000	Maximum number of tags the TBT can hold while merging (Default: 200000000).	Merges separate TBT files into a single, experiment-wide TBT file for all of the flow cell lanes of the experiment.

UNEAK/GBS	tbt2vcfPlugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3.	SNP calling.
		mnLCov	0.0	Minimum locus coverage (proportion of Taxa with a genotype) (Default: 0.0).	Option outputs SNPs covering the proportion of taxa (samples) with a genotype
		mnMAF	0.01	Minimum minor allele frequency (Default: 0.0).	Option outputs SNPs passing the minimum minor allele frequency
UNEAK/GBS	MergeDuplicateSNP_vcf_Plugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3.	Finds duplicate SNPs in the input VCF file and merges them if they have the same pair of alleles
UNEAK/GBS	MergeTagsByTaxaFilesPlugin	s	300000000	Maximum number of tags the TBT can hold while merging (Default: 200000000).	Merges the separate TBT files into a single, experiment-wide TBT file for all of the flow cell lanes of the experiment.
		x	N/A	Merges tag counts of taxa with identical short names (Default: off).	Option merges the tag counts of taxa that have the same SampleName in the key file but were run on different flow cells, lanes or in the same lane but with different barcodes
UNEAK/GBS	tbt2vcfPlugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3.	SNP calling.
		mnLCov	0.0	Minimum locus coverage (proportion of Taxa with a genotype) (Default: 0.0).	Option outputs SNPs covering the proportion of taxa (samples) with a genotype

		mnMAF	0.01	Minimum minor allele frequency (Default: 0.0).	Option outputs SNPs passing the minimum minor allele frequency
UNEAK/GBS	MergeDuplicateSNP_vcf_Plugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3.	Finds duplicate SNPs in the input VCF file and merges them if they have the same pair of alleles

Table S3 Posterior membership value assigned for all genotypes to distinguish into the respective subpopulation cluster of finger millet.

Genotype number	Subpopulation1	Subpopulation2	Subpopulation3
1	8.64E-16	1	1.29E-14
2	5.87E-19	1	5.46E-18
3	0.999982496	7.42E-06	1.01E-05
4	1.10E-14	1	2.04E-14
5	1.09E-17	1	9.66E-17
6	1.42E-15	1	4.33E-13
7	0.739885113	0.259225792	0.000889095
8	4.15E-11	4.60E-16	1
9	0.999999754	2.59E-14	2.46E-07
10	0.999999344	3.24E-13	6.56E-07
11	0.999999999	7.75E-16	6.57E-10
12	0.999999685	8.86E-14	3.15E-07
13	0.001541175	6.58E-11	0.998458825
14	8.27E-06	1.40E-11	0.999991729
15	3.67E-11	1	7.57E-11
16	2.58E-05	2.77E-11	0.999974234
17	5.14E-05	2.28E-06	0.999946351
18	0.002286052	0.925568198	0.072145751
19	3.03E-13	1	9.82E-13
20	9.12E-13	1	8.61E-12
21	2.97E-20	1	4.08E-19
22	9.94E-13	1	1.29E-11
23	4.37E-11	6.69E-16	1
24	2.78E-10	7.20E-16	1
25	0.007120601	1.37E-11	0.992879399
26	1.23E-20	1	2.63E-19
27	5.93E-18	1	1.21E-17
28	0.999999996	5.18E-15	3.85E-09
29	0.999999998	1.15E-18	1.73E-09
30	0.999999998	2.12E-17	2.27E-09
31	1	1.63E-18	3.19E-10
32	0.999999999	1.82E-18	1.21E-09
33	0.999998732	6.53E-13	1.27E-06
34	3.16E-06	6.33E-07	0.999996206
35	0.999999635	1.33E-14	3.65E-07
36	0.999999997	1.77E-17	2.75E-09
37	1.25E-09	3.57E-14	0.999999999

38	2.94E-09	4.33E-14	0.999999997
39	1.14E-11	5.87E-17	1
40	1.38E-09	6.82E-15	0.999999999
41	5.76E-09	3.73E-15	0.999999994
42	2.33E-09	5.72E-14	0.999999998
43	3.61E-11	1.34E-16	1
44	1.11E-07	1.33E-12	0.999999889
45	5.62E-10	0.999998971	1.03E-06
46	2.20E-17	1	2.33E-16
47	2.23E-20	1	8.79E-19
48	1.00E-14	1	8.92E-13
49	0.95879039	2.24E-13	0.04120961
50	3.70E-14	1	2.09E-13
51	1	1.63E-19	5.97E-11
52	1.77E-10	1.53E-15	1
53	1.18E-10	3.54E-16	1
54	4.22E-09	0.999999	5.73E-07
55	0.091299	1.22E-11	0.908701
56	0.999377	0.000165	0.000458
57	3.93E-16	1	2.90E-15
58	4.12E-15	1	1.49E-14
59	2.55E-14	1	3.84E-14
60	1.29E-13	1	4.97E-13
61	6.12E-17	1	6.24E-16
62	7.18E-16	1	5.50E-15
63	1.17E-05	3.72E-12	0.999988
64	2.44E-11	1.44E-18	1
65	6.00E-11	3.79E-16	1
66	0.000585	1.33E-12	0.999415
67	1.08E-09	1.99E-16	1
68	0.999992	1.23E-12	8.47E-06
69	0.999997	3.32E-13	2.77E-06
70	6.08E-12	1.57E-16	1
71	0.978408	3.42E-09	0.021592
72	1	6.86E-13	1.31E-07
73	9.46E-15	1	1.45E-13
74	1	2.70E-14	3.32E-07
75	0.999838	2.05E-07	0.000161
76	1	3.87E-16	6.13E-10
77	1	5.68E-17	7.77E-09
78	1	1.51E-18	3.13E-10

79	1	6.46E-18	2.35E-09
80	1.53E-06	0.819597	0.180402
81	9.14E-12	1	6.32E-08
82	1.19E-10	0.999999	6.85E-07
83	1	1.61E-18	3.07E-09
84	2.03E-21	1	6.41E-20
85	1	4.69E-18	4.34E-09
86	2.00E-20	1	5.99E-19
87	0.999999	5.93E-14	6.86E-07
88	0.995914	1.26E-12	0.004087
89	1	2.43E-17	6.01E-09
90	1	1.96E-17	1.66E-09
91	1	2.14E-16	1.62E-09
92	1	2.40E-18	3.69E-09
93	1	4.47E-15	4.01E-08
94	1	1.59E-12	3.11E-07
95	0.571263	7.70E-11	0.428737
96	2.26E-07	1.40E-13	1
97	1.90E-05	1.12E-11	0.999981
98	1	1.05E-17	9.50E-09
99	1	2.28E-17	6.03E-09
100	4.56E-14	1	2.46E-13
101	1	1.67E-17	4.21E-08
102	1	2.97E-19	1.21E-09
103	5.39E-05	0.003509	0.996437
104	0.999999	4.09E-14	1.43E-06
105	1	3.79E-18	1.26E-09
106	1	7.31E-16	7.06E-10
107	1	5.24E-18	3.04E-09
108	1	3.76E-14	2.72E-07
109	0.999989	2.93E-13	1.15E-05
110	1	1.37E-16	8.83E-10
111	1	6.85E-18	4.73E-09
112	1	1.54E-15	2.52E-09
113	1	7.25E-16	3.00E-08
114	1	6.19E-18	5.19E-09
115	2.04E-11	2.99E-18	1
116	0.275007	1.24E-10	0.724993
117	1.33E-05	1.91E-11	0.999987
118	1.18E-06	3.76E-12	0.999999
119	5.65E-11	4.83E-16	1

120	1.46E-11	8.49E-17	1
121	0.999999	6.52E-13	8.16E-07
122	1.01E-09	0.999998	2.46E-06
123	3.31E-12	1	8.75E-09
125	8.91E-11	3.80E-16	1
126	2.08E-18	1	8.08E-18
130	1.19E-17	1	1.91E-15
134	4.47E-14	1	1.65E-13
145	0.99993	3.37E-06	6.62E-05
146	4.67E-17	1	3.72E-16
152	1	1.12E-15	1.76E-07
155	1.65E-19	1	4.05E-18
166	2.45E-14	1	1.08E-12
182	4.12E-16	1	2.41E-14
185	1	5.96E-14	2.19E-07
187	0.033256	8.67E-12	0.966744
125	8.91E-11	3.80E-16	1
126	2.08E-18	1	8.08E-18
130	1.19E-17	1	1.91E-15
134	4.47E-14	1	1.65E-13
145	0.99993	3.37E-06	6.62E-05
146	4.67E-17	1	3.72E-16
152	1	1.12E-15	1.76E-07
155	1.65E-19	1	4.05E-18
166	2.45E-14	1	1.08E-12
182	4.12E-16	1	2.41E-14
185	1	5.96E-14	2.19E-07
187	0.033256	8.67E-12	0.966744
203	1	6.83E-16	4.31E-08
209	1	5.73E-17	1.60E-08
214	0.999999	7.23E-13	6.59E-07
215	0.999999	6.93E-13	1.22E-06
216	1	6.96E-15	8.42E-08
219	0.999997	7.05E-13	2.87E-06
223	1.79E-06	1.43E-11	0.999998
224	0.135235	6.99E-10	0.864765
233	0.003248	6.50E-11	0.996752
240	1	2.13E-17	3.11E-09
241	3.29E-14	1	2.66E-11
246	0.001396	9.89E-11	0.998604
249	3.71E-05	4.00E-12	0.999963

253	3.49E-10	1	9.37E-11
254	0.990509	2.73E-08	0.009491
259	0.988208	3.32E-08	0.011792
260	9.68E-19	1	1.15E-16
261	4.26E-21	1	1.15E-19
262	5.32E-14	1	3.93E-14
263	1.61E-09	1	2.35E-07
264	2.73E-19	1	5.21E-18
265	2.75E-15	1	1.19E-12
266	2.28E-13	1	4.33E-12
275	6.30E-13	1	1.63E-12
283	0.004519	5.30E-09	0.995481
288	4.11E-11	6.13E-16	1
302	1.01E-05	1.10E-13	0.99999
303	1	1.24E-12	3.06E-07
304	7.29E-13	1	1.24E-12
305	1	8.67E-16	2.68E-09
306	1	8.86E-17	1.36E-08
308	1	5.22E-15	7.27E-08
309	0.998909	6.51E-15	0.001091
331	1	1.44E-17	2.71E-09
362	0.002033	3.18E-12	0.997967
363	3.11E-10	2.58E-16	1
368	1.86E-10	6.96E-17	1
394	3.15E-20	1	1.90E-18
401	1	1.89E-16	4.68E-07
415	0.999996	1.92E-13	3.72E-06
440	5.63E-08	1	6.51E-10
455	1	1.70E-16	2.09E-08
459	1.73E-11	1.53E-16	1
469	0.229688	0.770306	6.39E-06
491	6.04E-14	1	4.61E-13
493	5.33E-18	1	5.47E-17
496	1	7.04E-19	2.14E-09
497	0.014593	4.05E-05	0.985367
502	1.23E-11	1	3.71E-11
514	1.73E-10	3.34E-16	1
515	4.59E-11	3.92E-15	1
528	2.67E-07	1.45E-13	1
530	4.53E-05	5.15E-12	0.999955

Table S4 The distribution of six grain micronutrients and total protein content in grains of finger millet germplasm collection.

Inventory	Accession name/number (IE)	Protein (%w/w)	Calcium (mg/100g)	Iron (mg/100g)	Zinc (mg/100g)	Magnesium (mg/100g)	Potassium (mg/100g)	Sodium (mg/100g)
1	501	10.31	350.63	8.513	1.001	147.28	251.25	13.63
2	518	9.06	354.73	7.411	1.579	158.85	356.63	9.98
3	1055	12.38	409.23	9.671	1.471	149.64	325.99	9.94
4	2034	11.31	278.85	4.459	1.696	122.2	432.49	8.07
5	2042	9.38	337.96	6.928	1.631	154.1	349.05	7.45
6	2217	9.06	285.19	6.26	1.656	129.58	348.56	14.68
7	2296	9.94	296.31	6.683	1.345	122.7	357.16	12.14
8	2312	9.75	278.95	6.008	1.659	126.28	446.14	11.37
9	2430	9.44	262.31	4.914	1.596	125.7	517.47	11.78
10	2437	6.63	318.19	6.479	1.517	130.87	401.89	10.95
11	2457	8.44	332.71	4.328	1.636	112.99	484.92	13.28
12	2589	7.69	242.9	5.837	1.117	100.55	660.91	19.88
13	2606	10.63	308.26	4.512	1.19	146.66	468	15.3
14	2619	9.31	357.77	5.652	1.792	147.11	424.64	16.08
15	2821	8.88	327.24	7.061	1.419	139.27	356.04	9.57
16	2871	8.75	354.52	6.132	1.305	139.51	514.72	13.3
17	2872	7.19	340.19	4.758	2.451	123.96	502.19	16.77
18	2911	9.56	292.52	5.812	1.338	113.43	399.07	9.73
19	2957	10.38	380.33	6.547	1.58	185.47	268.63	10.14

20	3045	7.88	346.72	4.548	1.102	108.32	281.99	7.19
21	3077	10.25	341.61	4.893	1.55	140.89	312.85	18.43
22	3104	8.25	317.81	4.306	1.346	137.99	332.25	12.75
23	3317	6.75	297.88	4.805	1.451	133.1	356.35	9.98
24	3391	6.81	258.34	3.406	1.51	125.03	452.74	14.78
25	3392	7.00	310.65	4.452	1.513	128.11	390.98	14.82
26	3470	7.81	354.29	4.487	1.842	142.51	354.04	13.21
27	3475	6.50	377.79	4.614	1.958	141.16	356.23	11.54
28	3614	6.81	319.11	5.651	1.394	137.66	344.21	8.25
29	3721	7.00	344.24	3.422	1.691	124.21	439.52	5.97
30	3945	7.06	308.56	6.354	1.503	127.21	399.19	11.79
31	3952	7.31	311.65	6.794	1.486	133.07	365.88	10.03
32	3973	5.63	331.27	3.99	1.476	133.01	342.15	13.59
33	4028	6.06	321.6	4.756	1.36	136.73	339.99	12.38
34	4057	6.44	354.22	4.955	1.436	125.66	322.38	9.78
35	4073	6.50	321.23	5.346	1.436	128.72	354.42	8.02
36	4121	8.19	308.7	6.289	1.588	130.11	315.57	8.5
37	4329	7.69	298.03	6.998	1.383	135.22	304.94	7.83
38	4491	7.06	362.29	5.587	1.502	135.21	300.13	6.13
39	4497	5.63	292.62	4.586	1.287	145.21	366.97	9.12
40	4545	9.94	300.19	5.299	1.514	126.84	421.95	12.51
41	4565	6.06	289.95	4.791	1.264	138.98	365.81	7.51

42	4570	7.69	327.3	7.894	1.185	125.7	278.26	10.04
43	4622	8.44	279.16	5.778	1.262	125.14	439.42	13.92
44	4646	6.88	309.54	5.446	1.181	124.03	296.52	7.57
45	4671	8.13	327.54	5.273	1.513	128.46	296.84	5.99
46	4734	8.19	331.01	11.218	2.704	137.75	275.73	18.51
47	4757	6.31	347.29	8.066	1.204	120.62	345.68	14.63
48	4759	7.63	355.27	8.387	1.21	143.36	323.83	39.1
49	4797	9.38	286.01	7.687	1.448	113.83	342.28	15.94
50	4816	8.38	254.5	6.806	1.464	103.49	535.78	18.94
51	5066	5.19	308.52	8.135	1.218	132.2	376.28	12.39
52	5091	7.00	338.21	7.699	1.184	136.62	350.46	10.4
53	5106	7.19	301.07	7.611	1.698	141.38	321.81	11.84
54	5201	6.56	397.84	15.315	1.634	153.71	308.59	14.08
55	5306	7.44	309.4	5.283	1.311	123.33	343.51	10.71
56	5367	8.88	340.31	6.153	1.374	136.18	288.12	9.87
57	5537	6.63	290.91	4.334	1.334	128.5	334.24	10.79
58	5870	8.25	264.69	5.576	1.48	126.93	407.06	13.6
59	6059	8.88	304.01	6.117	1.915	140.36	247.8	17.21
60	6154	6.63	287.41	6.489	1.127	114.67	318.66	12.75
61	6165	8.25	322.05	5.333	1.194	138.32	304.8	9.12
62	6221	7.13	271.3	5.054	1.755	132.19	363.16	14.09
63	6240	5.25	315.72	4.592	1.236	137.13	411.5	15.65

64	6294	6.50	342.22	5.329	1.278	144.19	336.85	7.29
65	6326	8.50	314.08	8.142	1.287	137.99	340.11	15.49
66	6337	6.38	313.76	10.669	1.727	150.4	268.4	19.1
67	6350	8.88	271.02	9.459	1.04	143.28	525.43	22.38
68	6421	8.38	306.87	8.29	2.144	124.93	407.73	16.63
69	6473	10.63	302.35	9.319	1.739	142.93	350.84	15.91
70	6514	6.44	305.6	6.615	1.266	144.69	355.2	12.39
71	6533	8.25	336.42	8.621	1.184	155.89	364.4	32.68
72	7018	5.31	283.17	9.791	1.315	133.4	309.5	10.35
73	7081	7.19	342.24	4.557	1.264	147.24	318.04	15.08
74	7320	6.38	283.62	5.006	1.543	140.22	396.51	12.47
75	7508	10.94	307.95	8.482	1.65	137.61	352.8	17.67
76	ACC#32	11.50	284.14	5.868	2.705	152.14	376.62	6.96
77	Acc. # 29 FMB/01 WK	8.56	282.64	5.004	2.193	139.37	386.61	16.77
78	Acc. # 32 FMB/01 WK	6.31	287.89	3.259	1.018	138.84	347.63	13.26
79	Acc.# 25 FMB/01 WK	7.00	321.01	4.533	1.386	115.13	345.53	9.28
80	AICSMIP # 3	10.13	364.57	4.497	1.813	139.25	306.72	9.2
81	AICSMIP # 58	5.00	334.12	5.658	1.403	144.81	409.09	24.96
82	AICSMIP # 9	5.88	323.84	4.482	1.395	129.72	313.34	24.92
83	ENDING	9.81	342.59	6.906	2.244	148.35	422.75	18.4
84	ENGENY	7.50	348.88	5.558	1.348	146.39	317.91	28.48
85	Gulu E	9.06	241.76	4	1.873	124.91	436.79	11.37

86	HR 374	5.75	313.34	3.704	1.425	136.23	301.33	17.77
87	Ikhulule	10.00	300.58	5.208	1.712	137.05	360.24	14.3
88	KNE # 1015	8.88	295.04	4.854	2.179	150.61	390.72	12.46
89	KNE # 1034	7.13	275.83	9.528	1.959	128.89	484.38	12.05
90	KNE # 1063	9.56	278.91	14.235	2.396	142.76	437.67	15.23
91	KNE # 1124	6.13	340.53	4.296	2.026	122.97	450.68	8.96
92	KNE # 1149	6.75	307.99	2.461	1.901	151.73	325.32	12.23
93	KNE # 392	9.06	314.26	5.589	2.089	126.49	382.47	14.75
94	KNE # 434	9.50	279.52	5.614	1.662	118.09	515.07	11.27
95	KNE # 622	7.00	252.13	4.209	1.708	124.74	484.61	42.84
96	KNE # 624	8.81	387.58	5.692	2.608	147.02	562.59	8.06
97	KNE # 628	8.88	199.82	3.438	1.406	105.74	481.68	15.53
98	KNE # 629	8.00	343.95	6.509	1.965	148.05	338.64	15.71
99	KNE # 648	6.50	301.74	4.042	1.622	129.68	410.8	19.05
100	KNE # 669	6.69	243.59	3.868	1.37	117.95	386.65	32.41
101	KNE # 688	6.56	295.17	4.531	1.308	121.19	280.18	19.2
102	KNE # 689	6.81	269.59	4.179	2.348	130.99	286.68	7.02
103	KNE # 689	8.75	317.06	4.535	1.622	138.46	355	7.41
104	KNE # 741	9.63	349.2	5.856	1.779	143.98	303.16	16.55
105	KNE # 758	9.00	249.13	5.456	1.714	114.31	375.77	14.51
106	KNE # 814	5.56	328.16	3.94	1.442	112.33	283.9	8.56
107	KNE 1098	8.13	346.81	5.632	1.89	143.05	327.72	13.57

108	KNE 409	5.25	296.85	3.897	1.33	128.95	375.21	12.7
109	KNE 479	7.06	307.06	3.541	1.584	130.68	298.23	31.82
110	KNE 796	10.25	260.19	4.428	1.854	113.44	394.69	11.46
111	KNE 884	9.38	264.67	5.978	1.747	106.38	377.98	8.32
112	Nakuru FM 1	6.50	330.8	8.111	1.214	141.58	314.05	7.92
113	Okhale-1	6.00	335.4	6.897	1.535	151.91	320.49	10.62
114	P 224	8.00	282.81	4.166	1.25	128.1	301.42	9.23
115	S # 414 GRU/ICRISAT	9.25	312.63	5.136	0.981	137.49	412.06	24.45
116	S # 589 GRU/ICRISAT	8.38	343.86	4.846	0.933	135.76	519.99	24.01
117	S # 70 SADC/ICRISAT	7.69	281.21	5.035	1.609	119.04	378.49	10.3
118	S # 94 SDFM 1752	6.94	326.68	8.816	1.98	135.35	427.76	14.07
119	SDFM 1702	6.00	282.56	2.94	1.569	136.04	346.33	7.69
120	U 15	11.44	236.02	4.151	2.152	166.85	362.56	6.36
121	Uganda Coll. # 3 Sel.10	9.13	289.48	6.774	1.512	124.32	286.74	6.52
122	VL 137	5.75	311.78	6.257	1.469	139.28	238.24	9.71
123	VL 224	9.19	287.77	4.386	1.843	147.44	292.47	23.89
125	9	5.25	273.95	4.519	1.157	116.04	399.45	14.03
126	61	8.88	364.39	4.194	1.242	136.01	306.07	10.81
130	546	10.25	357.04	4.872	1.488	145.15	284.43	17.44
134	595	10.63	363.07	7.514	1.571	155.18	272.05	9.84
145	872	9.06	345.57	6.414	2.095	152.2	348.92	9.53
146	886	8.44	330.6	3.994	1.749	135.05	337.33	11.91

152	1023	7.56	300.91	6.337	1.603	123.85	378.33	13.01
155	2008	8.38	382.49	5.583	1.632	130.45	329.02	11.53
166	2108	6.69	380.47	3.886	1.548	119.97	284.78	9.81
182	2293	8.13	359.59	3.478	1.555	143.68	313.32	16.61
185	2341	7.94	244.07	3.578	1.554	101.35	501.05	11.12
187	2354	9.06	237.38	4.186	1.553	117.1	441.37	10.81
203	2500	8.75	260.71	4.468	1.649	117.25	602.62	12.46
209	2564	9.63	284.52	4.877	1.223	115.81	464.59	11.5
214	2581	6.50	322	5.373	1.093	118.2	589.39	25.54
215	2586	5.56	359.34	16.475	1.182	110.16	516.62	15.02
216	2587	5.81	283.29	4.176	0.956	130.56	483.68	14.71
219	2593	8.31	273.36	4.087	1.104	116.3	517.38	16.21
220	2608	-	-	-	-	-	-	-
223	2644	10.44	335.91	4.82	1.47	118.08	591.13	29.6
224	2645	8.25	317.1	4.007	1.15	123.37	499.2	23.93
233	2760	6.63	317.18	4.616	1.229	129.31	313.89	14.25
240	2825	8.88	311.1	3.984	1.245	135.36	347.72	9.22
241	2838	9.63	367.98	3.138	1.752	128.89	597.27	13.42
246	2869	6.75	379.57	4.043	1.228	149.61	383.79	18.65
249	2896	5.69	321.25	4.258	1.979	115.32	343.27	5.46
253	2971	5.94	328.54	5.136	1.598	134.67	549.87	4.97
254	2983	6.50	339.57	5.006	1.652	128.75	556.83	16.86

259	3025	7.31	322.22	4.234	1.558	130.84	355.34	23.4
260	3028	6.94	341.53	3.561	1.685	128.41	256.39	11.01
261	3038	9.88	338.09	3.433	1.455	124.1	340.76	7.88
262	3046	7.63	328.37	5.6	1.355	108.84	557.93	12.25
263	3062	4.38	336.08	3.745	1.232	137.56	293.76	29.89
264	3066	10.00	361.75	4.583	1.544	122.42	327.1	8.61
265	3070	7.75	376.8	3.932	1.661	123.21	286.24	14.86
266	3073	6.50	311.52	3.597	1.725	124.97	341.54	8.85
275	3124	9.38	324.62	5.587	1.418	125.79	345.52	9.6
283	3196	9.63	288.89	3.898	1.621	122.87	373.81	15.75
288	3257	6.50	246.88	3.405	1.532	106.24	395.86	10.09
302	3443	6.88	288.51	5.909	1.845	133.07	432.61	8.07
303	3449	5.88	319.53	13.242	1.474	133.82	382.47	10.87
304	3450	9.63	299.4	3.863	1.774	144.83	349.18	10.32
305	3455	8.44	286.23	4.505	1.416	125.44	399.33	13.97
306	3477	5.75	358.27	3.769	1.553	129.05	425.66	12.08
308	3489	5.50	373.28	3.737	1.443	128.95	345.39	13.31
309	3492	6.00	340.01	3.789	1.483	132.47	331.24	10.09
331	3738	9.13	304.8	4.638	1.386	142.44	406.52	15.46
362	4218	10.69	336.33	5.398	1.668	145.4	281.38	11.59
363	4220	5.50	285.53	4.233	1.421	119.9	438.42	8.84
368	4287	7.13	297.28	3.746	1.287	123.89	442.38	8.84

394	4826	8.56	333.32	4.882	1.452	140.76	372.95	12.94
401	4916	10.25	287.64	4.967	2.284	145.17	313.88	9.45
415	5124	9.81	278.64	5.309	2.292	137.27	355.27	9.59
440	5331	7.81	317.73	4.557	1.519	123.39	425.53	15.26
455	5485	8.00	237.29	4.782	1.223	116.12	351.51	14.87
459	5517	10.56	282.83	10.64	2.758	151.07	380.66	7.68
469	5672	6.56	317.26	5.057	1.511	128.22	344.22	12.04
491	5992	8.31	363.09	4.713	1.832	137.65	354.29	9.87
493	6013	7.81	334.9	5.479	1.567	142.74	283.41	12.33
496	6029	11.00	373.02	3.215	2.37	134.27	286.04	6.92
497	6033	8.44	276.23	4.912	1.563	153.24	372.36	14.67
502	6112	7.44	217.83	4.793	2.142	108.22	432.26	8.15
514	6300	6.81	344.41	4.837	1.251	147.37	314.17	16.47
515	6313	7.44	306.16	3.937	1.601	113.45	385.52	16.95
528	6528	8.63	308.09	6.713	1.935	139.09	387.15	15.53
529	6537	-	-	-	-	-	-	-
530	6541	7.38	409.71	9.889	1.885	132.58	310.76	7.81

Table S5 SNP dataset information on the sequence. The SNP base is marked in red.

> Iron_S1_5895347

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CAGCAGATCAATGGGGAATGCGAAGAACGAACCTGGTGCACCAGATGAACGTGTCCAGGAGCAG

> Iron_S1_30253617

CAGCTTCTAATTTTGCAGGAGTCGTGAAACACAACTTTGCTTACATGCATTTTTGGGAGATCAT

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> Iron_S1_16501848

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> Iron_S1_37285642

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>Iron_S1_29108559

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>Iron_S1_46868946

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>Iron_S1_30508238

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>Iron_S1_3940038
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Table S6 Annotation results of the dataset based on syntenic relationship among monocots using *in silico* comparative genomics.

Trait	Marker ID	Database	Hit ID	Matching Hit	E-Value	Putative Function	Reference
Iron	S1_30253617	NCBI	XM_004967040.2	*Setaria italica* uncharacterized LOC101766508 (LOC101766508), mRNA	5.00E-09	No apical meristem-associated C-terminal domain is associated with Fe and Zn remobilization	Ricachenevsky et al., 2013
Iron	S1_55920039	NCBI	XM_002458644.2	PREDICTED: *Sorghum bicolor* RING-H2 finger protein ATL74 (LOC8085401), mRNA	3.00E-11	Molecular function: metal ion binding	http://www.uniprot.org/uniprot/Q9LZV8
Iron	S1_55628636	NCBI	NM_001153123.1	*Zea mays* uncharacterized LOC100280191 (LOC100280191), mRNA	3.00E-12	Putative leucine-rich repeat receptor protein kinase family protein involved in regulating heavy metal accumulation	Ye et al., 2017
Iron	S1_23343453	NCBI	XM_004969850.3	*Setaria italica* probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial (LOC101754224), mRNA	3.00E-12	Accumulation and trafficking of intracellular iron in mammals	Devireddy et al., 2010; Liu et al., 2014
Iron	S1_46868946	NCBI	XM_015779399.1	*Oryza sativa* Japonica Group cactin-like (LOC107275754), mRNA	4.00E-04	Role in binding metal ions	Lin et al., 2000

Iron	S1_2042517	Ensembl Plants	Et_s3897-0.3-1.mrna1	*Ergostis tef* Et_s3897-0.3-1.path1	2.40E-03	Glycosyltransferase 34	Ensembl Plants
Iron	S1_47532644	Phytozome	-	*Panicum halli* Chromosome 3	8.00E-04		
Iron	S1_30674733	NCBI	XM_010230346.3	*Brachypodium distachyon* putative potassium transporter 8 (LOC100823609), transcript variant X4, mRNA	2.00E-13	Mineral transporter	
Iron	S1_33201053	Phytozome	-	*Oropetium thomaeum*_genomic_20141112_05	6.60E-05		
Iron	S1_22601238	NCBI	XM_004956895.3	*Setaria italica* protein Brevis radix-like 1 (LOC101769951), mRNA	1.00E-17	Root development	http://www.uniprot.org/uniprot/Q17TI5
Iron	S1_41020649	NCBI	KJ728522.1	*Zea mays* clone pUT6827 HB transcription factor (HB14) mRNA, partial cds	7.00E-20	Regulation of transcription	http://www.uniprot.org/uniprot/Q7XYR8
Iron	S1_43657254	NCBI	XM_004965844.3	*Setaria italica* aspartyl protease family protein At5g10770 (LOC101780935), mRNA	9.00E-19	Proteolytic enzyme	http://www.uniprot.org/uniprot/Q940R4
Iron	S1_47471042	NCBI	XM_020302967.1	*Aegilops tauschii subsp. tauschii*	3.00E-11		

				uncharacterized LOC109743882 (LOC109743882), mRNA			
Sodium	S1_47207745	Ensembl Plants	Et_s7702-0.5-1.mrna1	*Eragrostis tef* Et_s2224-1.73-1.path1	4.3E-14	LNK family (circadian rhythms and the photoperiodic regulation of flowering time)	http://www.ebi.ac.uk/interpro/entry/InterPro/IPR039928/
Sodium	S1_23925117	Phytozome	-	*Zea mays* PH207_chr05; Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase	9.80E-03	Metal ion binding	http://www.uniprot.org/uniprot/Q9NS00
Sodium	S1_53281655	Ensembl Plants	Et_s7379-1.39-1.mrna1	*Eragrostis tef* Et_s7379-1.39-1.path1	6.00E-10	Tetratricopeptide repeat (TPR); Important for tolerance to sodium chloride stress	Rosado et al., 2006
Sodium	S1_33945446	Ensembl Plants	Et_s2224-1.73-1.mrna1	*Eragrostis tef* Et_s7702-0.5-1.path1		Pentatricopeptide repeat family (RNA metabolism, reactive oxygen species generation and abiotic stress resistance)	Xu et al., 2018
Sodium	S1_55873457	Ensembl Plants	BGIOSGA022153-TA	*Oryza sativa* Indica group WAT1-related protein	7.00E-03	Transmembrane transporter activity	https://www.uniprot.org/uniprot/B8B1J0
Sodium	S1_5208938	Phytozome	-	*Zea mays* PH207 v 1.1 chr08	9.8E-4		
Potassium	S1_55418346	NCBI	XM_004981804.3	*Setaria italica* ankyrin repeat-containing protein At5g02620	2e-04	Crucial role in defense responses and growth and development	Vo et al., 2015.

				(LOC101768509), mRNA			
Potassium	S1_47042025	Phytozome	-	*Panicum virgatum* peroxidase precursor, putative, expressedts	5.4E-7	Metabolite associated with essential micronutrients	Welch and Shuman, 1995
Magnesium	S1_463458	Phytozome	-	*Setaria italica* scaffold_9	2.8E-04		
Calcium	S1_4620123	Phytozome	-	*Oryza sativa* subsp. japonica) Oropetium_20150105_18364A; Squamosa promoter-binding-like protein 5	3.4E-3	Trans-acting factor that promotes both vegetative phase change and flowering	https://www.uniprot.org/uniprot/Q9S758
Calcium	S1_44130155	Ensembl Plants	OB04G31600.1	*Oryza brachyantha* cdna chromosome:Oryza_brachyantha.v1.4b:4:17649575:17652174:-1	0.0062	Uncharacterized protein; biological process cell redox homeostasis	https://www.uniprot.org/uniprot/J3M185
Calcium	S1_5982733	NCBI	XM_025951302.1	*Panicum hallii* transcriptional corepressor SEUSS-like (LOC112885704), mRNA	6e-10	Calcium-dependent transactivator associated with development in mammals	Kashani et al., 2006

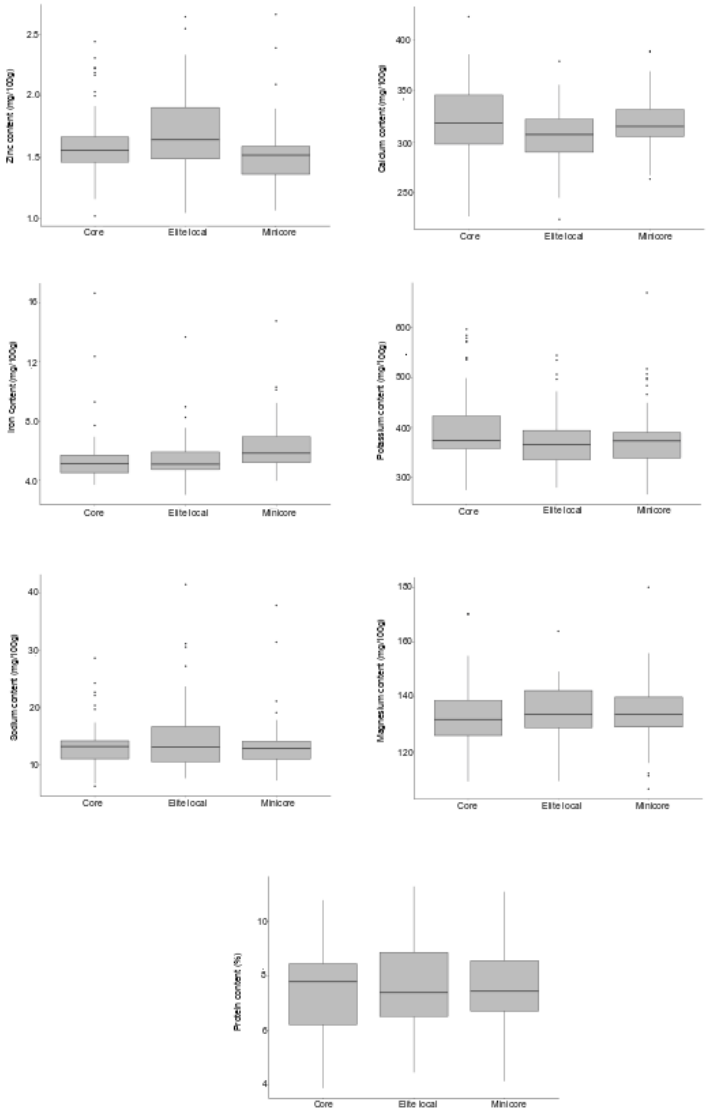

Fig. S1 Box Plot distributions for grain micronutrient and protein content in different groups of finger millet germplasm, *viz.*, core, minicore and elite local varieties.

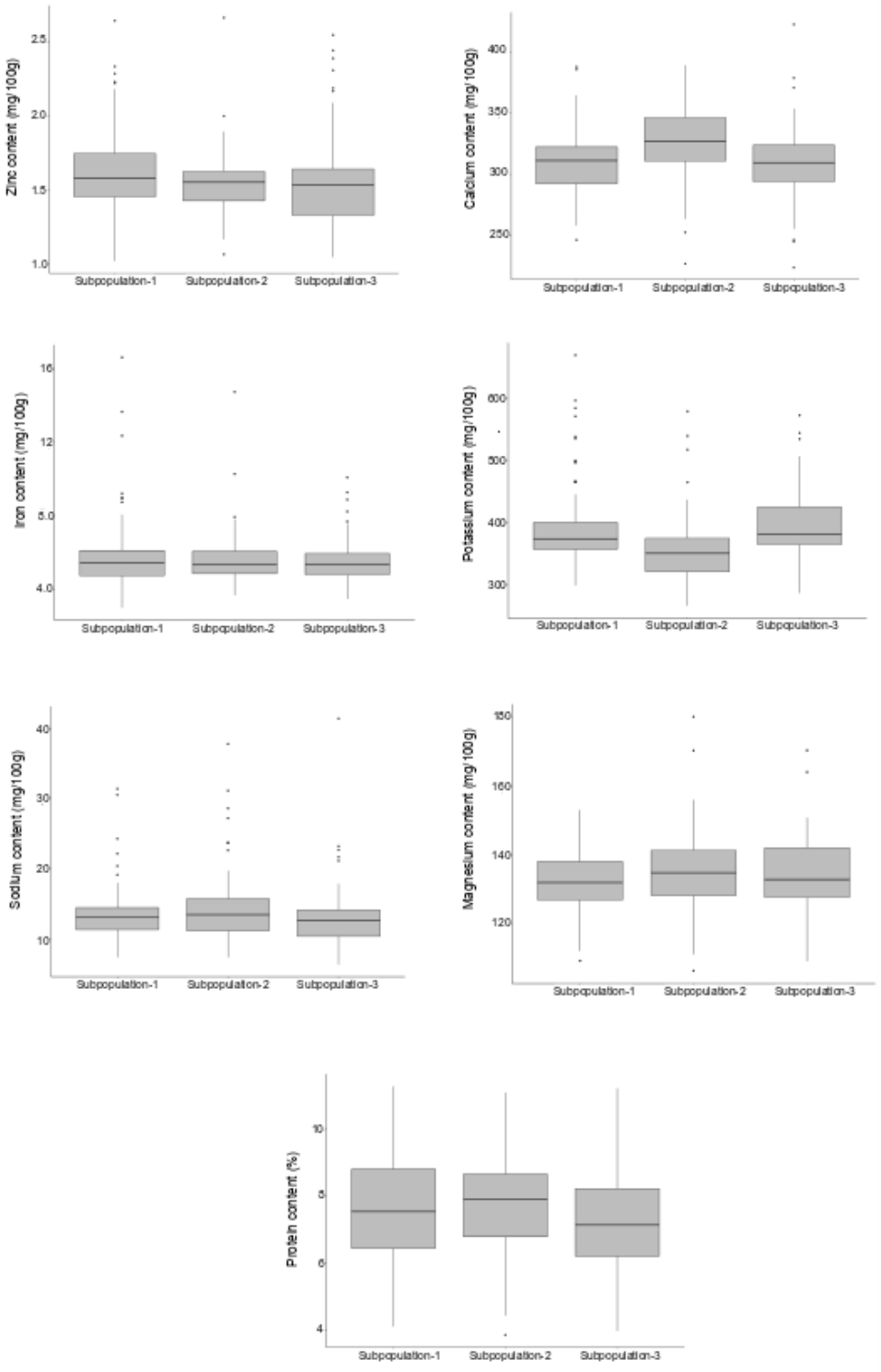

Fig. S2 Box Plot distributions for grain micronutrient and protein content in different subpopulations of finger millet germplasm, *viz.*, East African, Asian and South African.

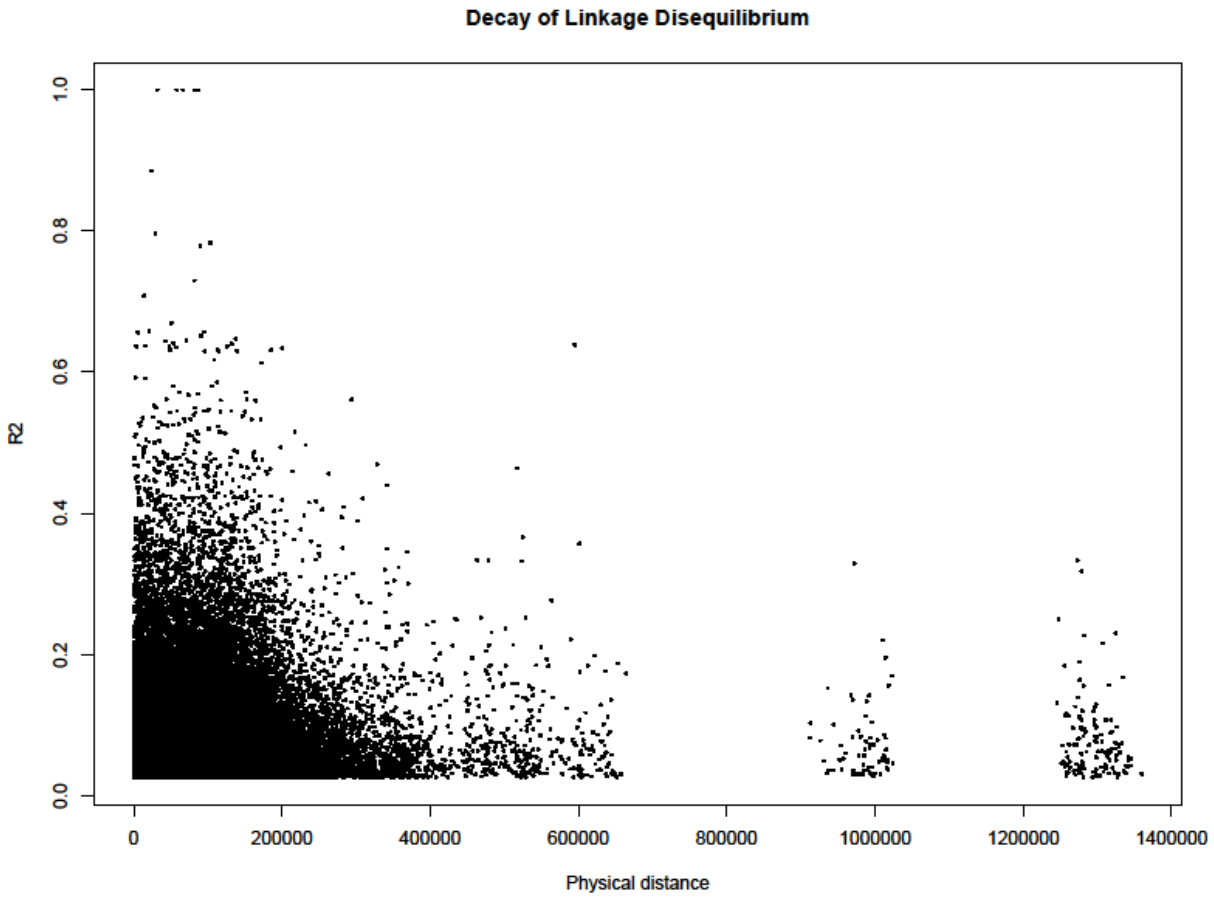

Fig. S3 Plot of genome-wide linkage disequilibrium (LD) decay. The plot shows pair-wise single-nucleotide polymorphism LD r2 values as a function of intermarker physical distance (bp).

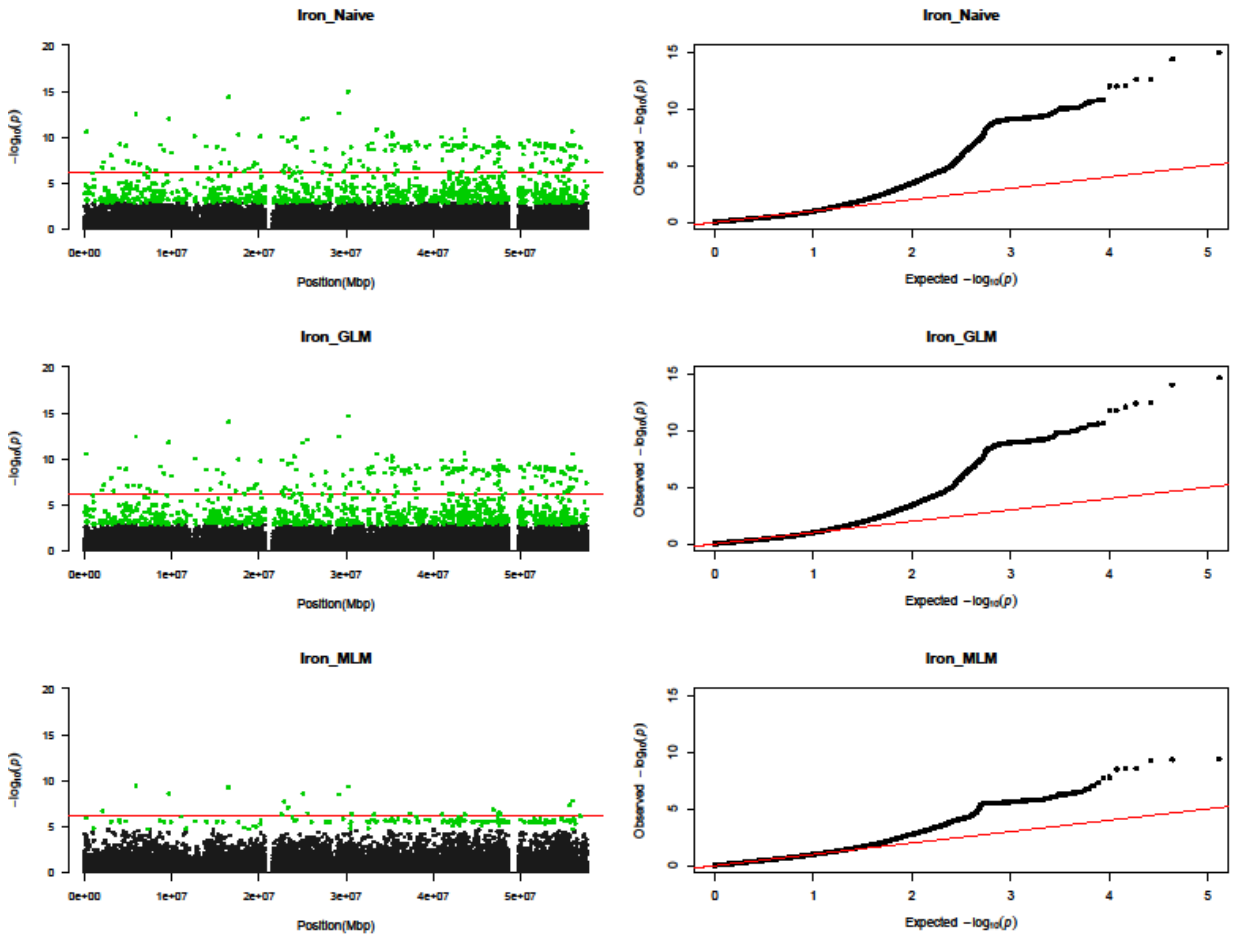

Fig. S4 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain iron content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.

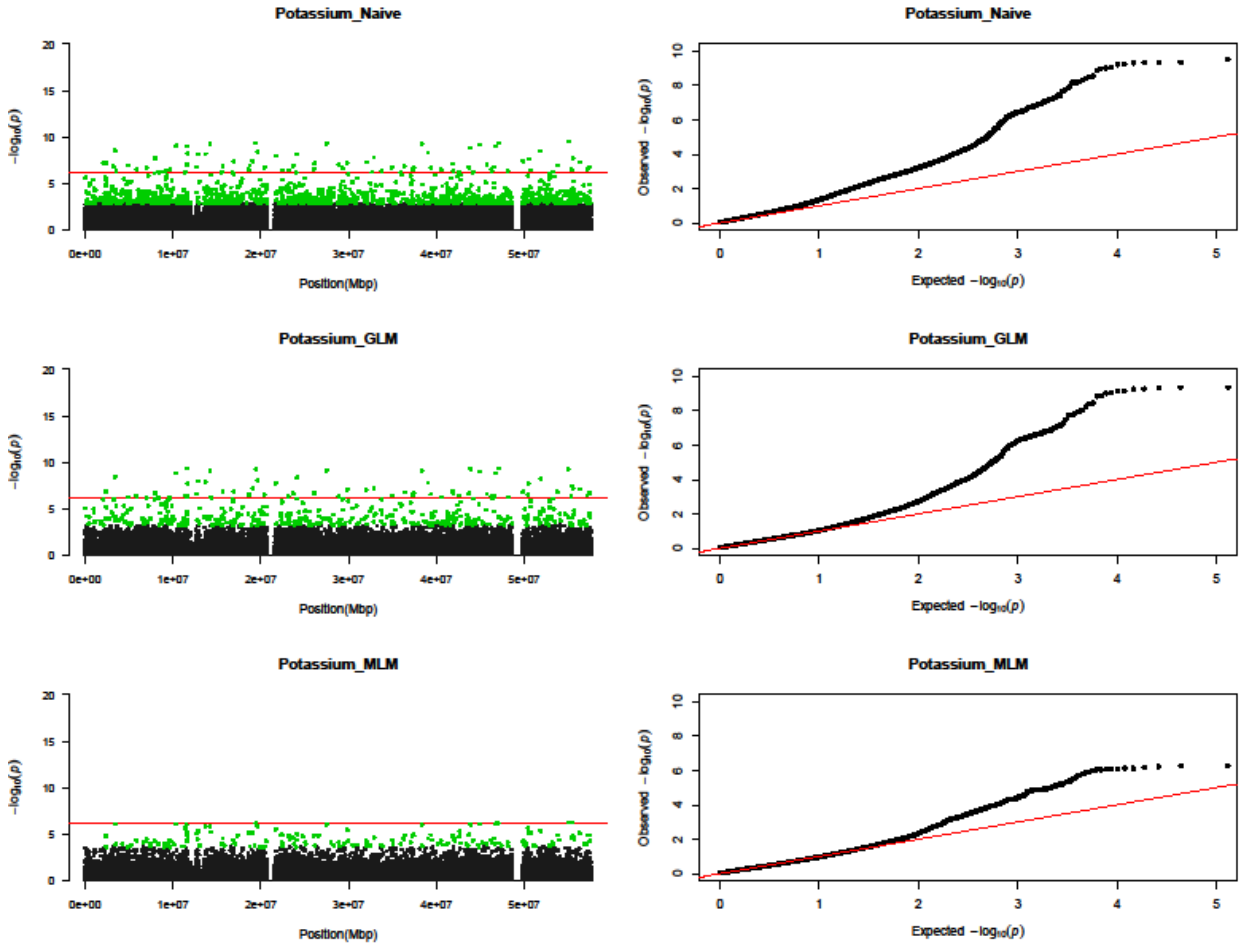

Fig S5 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain potassium content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.

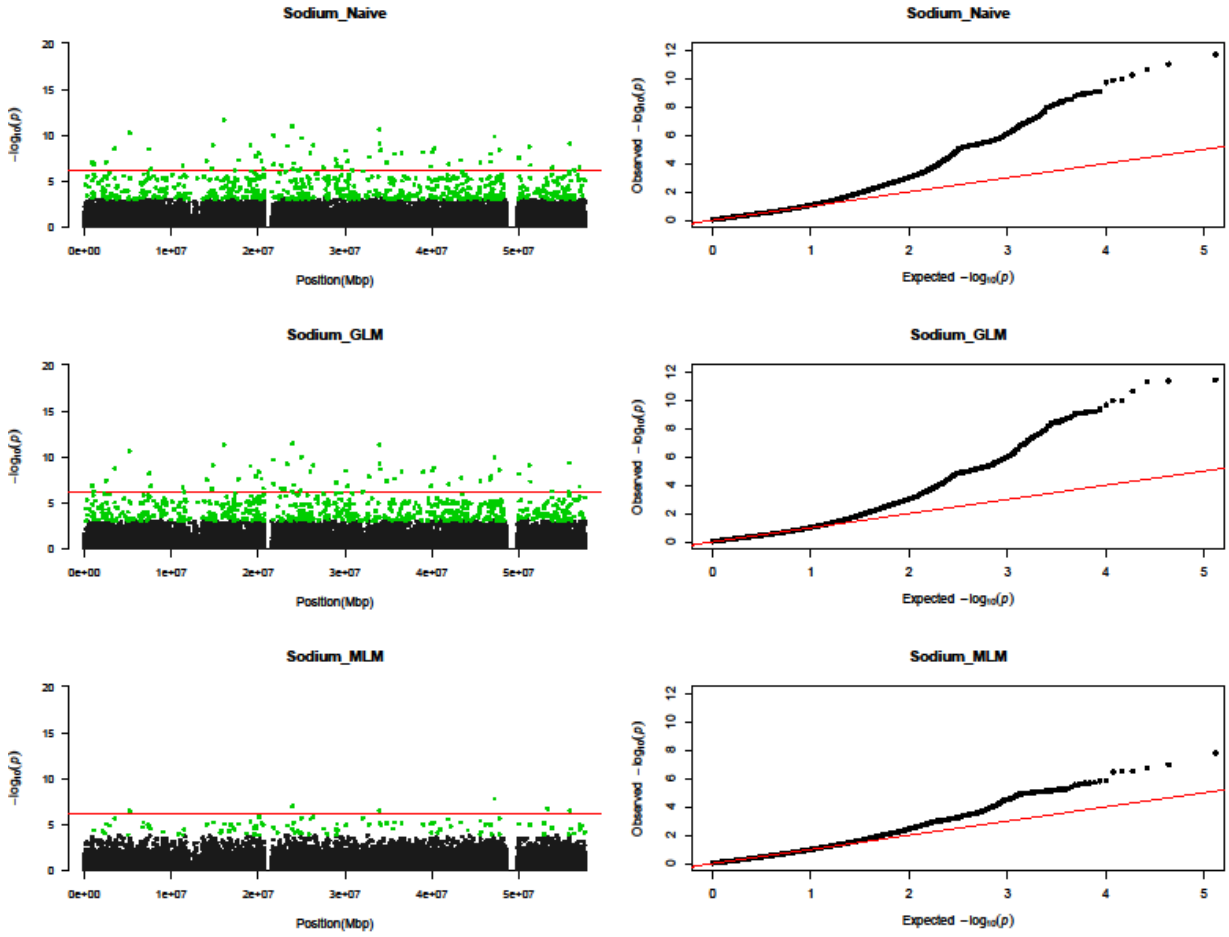

Fig. S6 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain sodium content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.

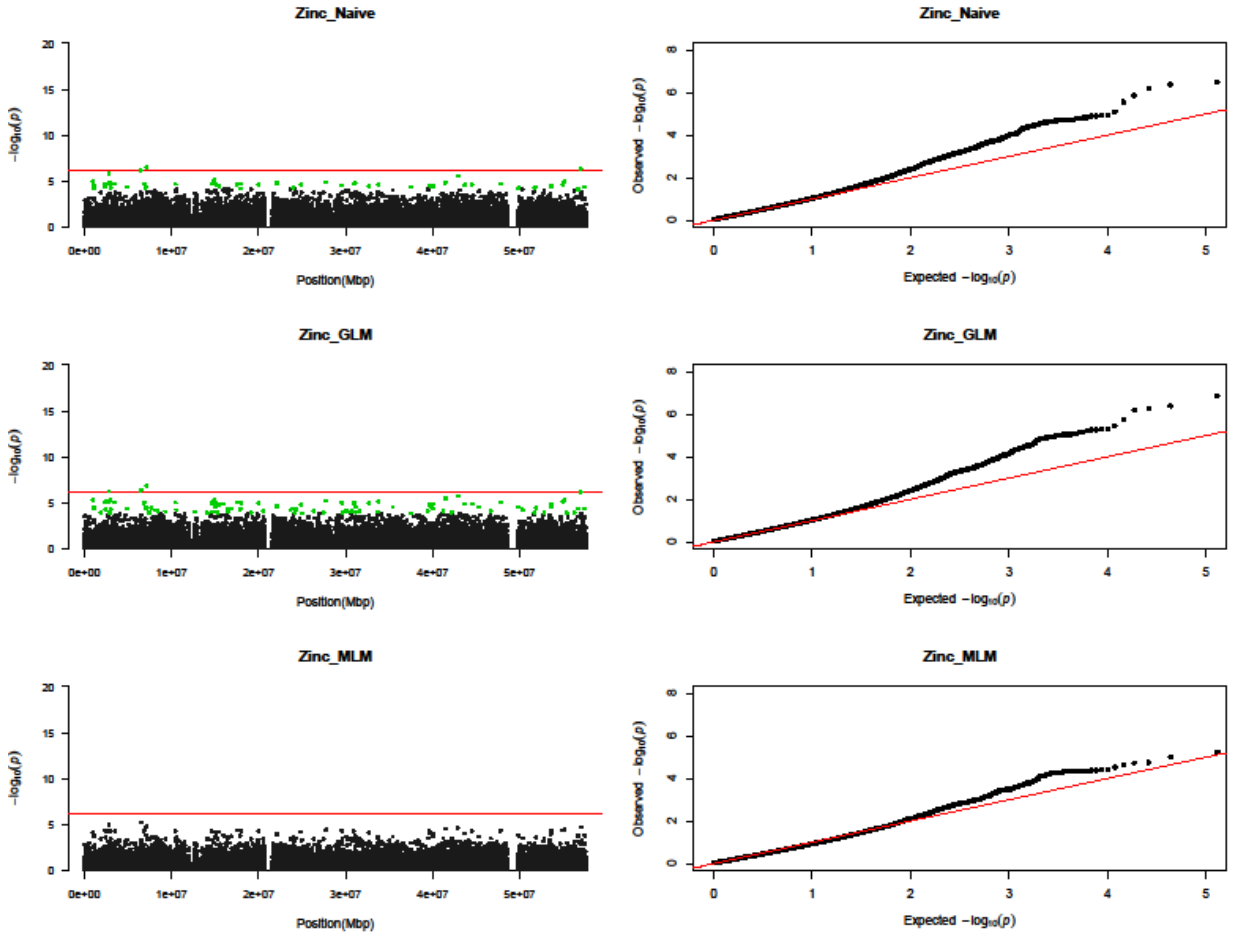

Fig. S7 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain zinc content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.

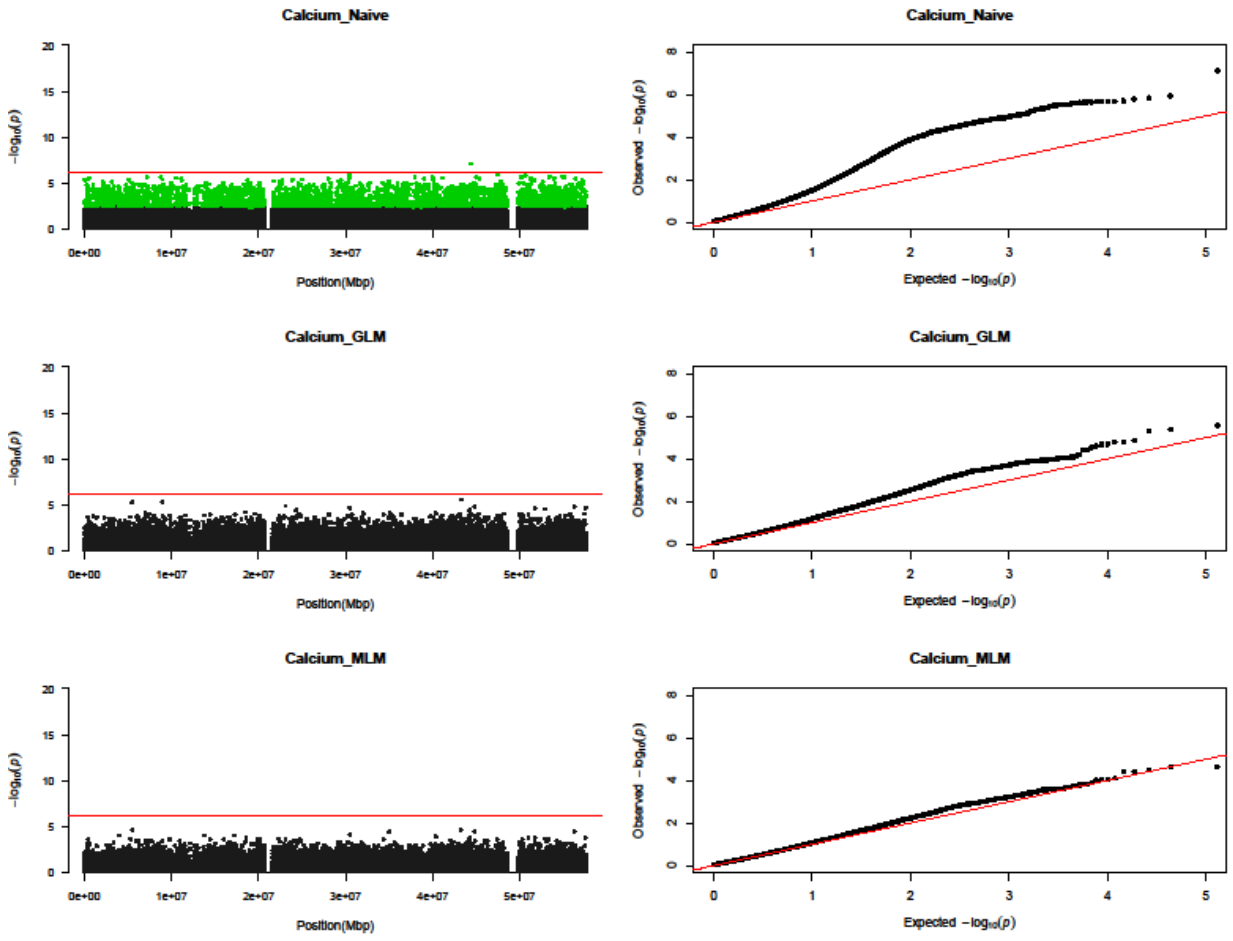

Fig. S8 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain calcium content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.

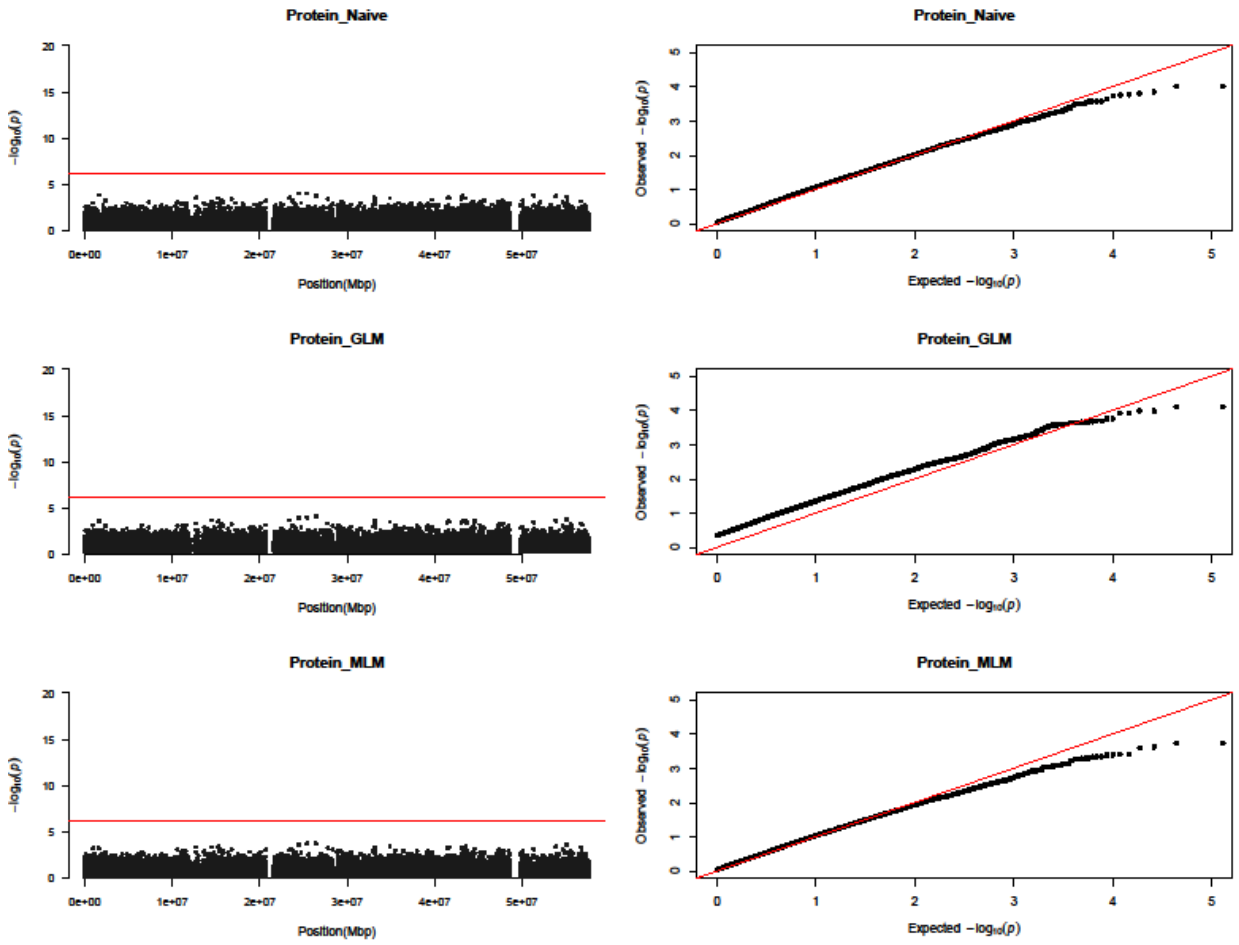

Fig. S9 Manhattan and corresponding quantile-quantile (QQ) plots of genome-wide association data showing −log10 P value vs. random position of SNP markers generated after relaxed filtering from the three models (a) Naïve (b) GLM (Q) (c) MLM (Q + K) for grain total protein content. In the Manhattan plots, significant SNPs ($P \leq 0.001$, FDR <0.1) are shown as circles in green, non-significant SNPs (FDR>0.1) are shown as black circles. The red horizontal line represents the Bonferroni threshold with an estimate of genome-wide P value at 6.81E-07.